What is claimed is:

1. A computer software program product, comprising computer readable memory and a computer software program stored on the memory, for calculating linkage disequilibrium values for individual pairs of gene loci for two or more gene polymorphism data groups and displaying results comparatively on a display monitor, said program comprising:

    a color output command for converting the linkage disequilibrium values for individual pairs of gene loci for a first gene polymorphism data group and those for a second gene polymorphism data group into a first color set and a second color set, each color set comprising colors with differently allocated saturation, brightness and density based on the linkage disequilibrium values, and for outputting the two color sets; and

    a comparative display command for displaying comparative results for the first and second color sets on a display monitor in such a way that comparison of the disequilibrium values between the first and second gene polymorphism data groups can be made.

2. The computer software program according to Claim 1, wherein said comparative display command produces compounded colors, each compounded color obtained by combining the color associated with each pair of gene loci in the first color set and the color associated with the corresponding pair of gene loci in the second color set, and displays an array of the compounded colors on the display monitor as comparative results for the linkage equilibrium values between the first and second gene polymorphism data groups .

3. The computer software program according to Claim 1, further comprising a linkage disequilibrium value calculation command for calculating the linkage disequilibrium values for individual pairs of gene loci for the first and second gene polymorphism data groups respectively.

4. The computer software program according to Claim 3, further comprising a command for reducing the number of gene loci to be processed.

5. The computer software program according to Claim 4, wherein said command for reducing the number of gene loci to be processed comprises:

a procedure for calculating information entropy for one or more gene loci; and

a procedure for determining the gene loci to be processed based on the information entropy.

6. The computer software program according to Claim 5, wherein the information entropy is given by all combinations of minor and major alleles among gene loci and their frequencies.

7. The computer software program according to Claim 5, wherein the value of the information entropy is used as the linkage disequilibrium value.

8. A computer software program product, comprising computer readable memory and a computer software program stored on the memory, for calculating linkage disequilibrium values for individual pairs of gene loci for two or more gene polymorphism data groups, said program comprising:

a command for reading data of a predetermined gene polymorphism data group from a data storage;

a command for calculating information entropy for one or more gene loci for the gene polymorphism data group;

a procedure for determining gene loci to be processed based on the information entropy; and

a command for calculating the linkage disequilibrium values for individual pairs of the gene loci that were determined to be processed and for outputting them for display.

9. The computer software program according to Claim 8, wherein the information entropy is given by all combinations of minor and major alleles among gene loci and their frequencies.

10. A computer implemented method for calculating linkage disequilibrium values for individual pairs of gene loci for two or more gene polymorphism data groups and displaying results comparatively on a display monitor, said method comprising:

a color output process of converting the linkage disequilibrium values for individual pairs of gene loci for a first gene polymorphism data group and those for a second gene polymorphism data group into a first color set and a second color set, each color set comprising colors with differently allocated saturation, brightness and

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density based on the linkage disequilibrium values, and for outputting the two color sets; and

a comparative display process of displaying comparative results for the first and second color sets on a display monitor in such a way that comparison of the disequilibrium values between the first and second gene polymorphism data groups can be made.

11. The method according to Claim 10, wherein said comparative display process is a process of producing compounded colors, each compounded color obtained by combining the color associated with each pair of gene loci in the first color set and the color associated with the corresponding pair of gene loci in the second color set, and of displaying an array of the compounded colors on the display monitor as comparative results for the linkage equilibrium values between the first and second gene polymorphism data groups .

12. The method according to Claim 10, further comprising a linkage disequilibrium value calculation process of calculating the linkage disequilibrium values for individual pairs of gene loci for the first and second gene polymorphism data groups respectively.

13. The method according to Claim 12, further comprising a process of reducing the number of gene loci to be processed.

14. The method according to Claim 13, wherein said process of reducing the number of gene loci to be processed comprises:

a process of calculating information entropy for one or more gene loci; and

a process of determining the gene loci to be processed based on the information entropy.

15. The method according to Claim 14, the value of the information entropy is used as the linkage disequilibrium value.

16. A computer software program product, comprising computer readable memory and a computer software program stored on the memory, for calculating linkage disequilibrium values for individual pairs of gene loci for two or more gene polymorphism data groups and displaying results comparatively on a display monitor, said program comprising:

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a subtraction value output command for obtaining subtraction values, each subtraction value obtained by subtracting the linkage disequilibrium value for each pair of gene loci of a second gene polymorphism data group from the linkage disequilibrium value for the corresponding pair of gene loci of a first gene polymorphism data group, and for outputting the subtraction values; and

a linkage disequilibrium value comparison display command for producing colors corresponding to the subtraction values and for displaying an array of the colors on the display monitor as the linkage disequilibrium value comparison between the first and second gene polymorphism data groups.

17. A computer implemented method for calculating linkage disequilibrium values for individual pairs of gene loci for two or more gene polymorphism data groups and displaying results comparatively on a display monitor, said method comprising:

a subtraction value output process of obtaining subtraction values, each subtraction value obtained by subtracting the linkage disequilibrium value for each pair of gene loci of a second gene polymorphism data group from the linkage disequilibrium value for the corresponding pair of gene loci of a first gene polymorphism data group, and of outputting the subtraction values; and

a linkage disequilibrium value comparison display process of producing colors corresponding to the subtraction values and of displaying an array of the colors on the display monitor as the linkage disequilibrium value comparison between the first and second gene polymorphism data groups.